

3 CTCGCTTGCA 15

RESULT 4

AAFS1541 standard; DNA; 15 BP.

AAFS1541;

30-MAR-2001 (first entry)

IGF-1 oligonucleotide #2501.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytosaric; dermatological; cardiant; vitruide; ophthalmological; keloid; skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

MO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000MO-AU000693.

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 77; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-145161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, seborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 13; DB 1; Length 15;

Best Local Similarity 53.8%; Pred. No. 1.8;

Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

AAFS1543 standard; DNA; 15 BP.

AAFS1543;

30-MAR-2001 (first entry)

IGF-1 oligonucleotide #2503.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytosaric; dermatological; cardiant; vitruide; ophthalmological; keloid; skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

MO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000MO-AU000693.

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 77; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-145161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, seborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 92.3%; Score 12; DB 1; Length 15;

Best Local Similarity 50.0%; Pred. No. 2.5;

Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

AAFS1539 standard; DNA; 15 BP.

AAFS1539;

43

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GenCore version 5.1.9
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OM nucleic - nucleic search, using SW model

Run on: September 1, 2006, 12:04:34 ; Search time 0.001 Seconds
(without alignments)
9.490 Million cell updates/sec

Title: us-09-847-601b-88

Perfect score: 13

Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 34 seqs, 365 residues

Total number of hits satisfying chosen parameters: 68

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 34 summaries

Database: rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	100.0	13	1	ABZ72849
2	13	100.0	15	1	AAFS1542
3	13	100.0	15	1	AAFS1540
4	13	100.0	15	1	AAFS1541
5	12	92.3	15	1	AAFS1543
6	12	92.3	15	1	AAFS1539
7	10	76.9	10	1	AAFS8544
8	9	69.2	10	1	AAFS1570
9	9	69.2	10	1	AAFS3016
10	9	69.2	10	1	AAFS467
11	9	69.2	10	1	AAFS4844
12	8.4	64.6	10	1	AAFS4839
13	8.4	64.6	10	1	AAFS2946
14	8.4	64.6	10	1	AAFS4256
15	8.4	64.6	10	1	AAFS36161
16	8.4	64.6	10	1	AAFS4800
17	8.4	64.6	10	1	AAFS38546
18	8.4	64.6	10	1	AAFS40425
19	8.4	64.6	10	1	ABK96059
20	8.4	64.6	10	1	AD113726
21	8.4	64.6	10	1	ADU50908
22	8.4	64.6	10	1	AAH63934
23	8.4	64.6	10	1	AAH63934
24	8.4	64.6	10	1	AAFS4140
25	8.4	64.6	10	1	AAFS2583
26	8.4	64.6	10	1	AAFS7269
27	8.4	64.6	10	1	AAFS8836
28	8.4	64.6	10	1	AAFS4254
29	8.4	64.6	10	1	AAFS4626
30	8.4	64.6	10	1	AAFS4668
31	8.4	64.6	10	1	AAFS4032
32	8.4	64.6	10	1	AAFS9588
33	8.4	64.6	10	1	AAFS40670

34 7 53.8 8 1 ABK29982

ALIGNMENTS

Hepatitis B virus

RESULT 1
ABZ72849
ID ABZ72849 standard; RNA, 13 BP.
XX
AC ABZ72849;
XX
DT 09-APR-2003 (first entry)
XX
DE IGF1 R21 ribozyme target sequence SEQ ID NO:88.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW opthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN W020028320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002MO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (VYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Claim 1; Page 80; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention
XX

SQ Sequence 13 BP; 1 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUCGUCUUGCA 13

DB 1 CUUCGUCUUGCA 13

RESULT 2

AAFS1542 AAF51542 standard; DNA; 15 BP.

AC AAF51542;

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #2502.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX Example 8; Page 77; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF5151 and AAF5153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 13; DB 1; Length 15;

XX Best Local Similarity 53.8%; Pred. No. 1.8;

Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUCGUCUUGCA 13

DB 1 CUUCGUCUUGCA 13

RESULT 3

AAFS1540 AAF51540 standard; DNA; 15 BP.

AC AAF51540;

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #2500.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

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CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF5151 and AAF5153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 13; DB 1; Length 15;

XX Best Local Similarity 53.8%; Pred. No. 1.8;

XX Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

XX 1 CUUCGUCUUGCA 13

XX :::::|||||

Db 3 CTGCTTTGCA 15

RESULT 4
AAFS1541
ID AAF51541 standard; DNA; 15 BP.
AC AAF51541;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #2501.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 8; Page 77; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX P45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, scleroderma, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, ptyriasis, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia

Query Match 100.0%; Score 13; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.8;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUCGUCUUGCA 13
Db 2 CTGCTTTGCA 14

RESULT 5

AAFS1543
ID AAF51543 standard; DNA; 15 BP.
XX
XX AAF51543;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #2503.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
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XX inflammation.
XX
XX Example 8; Page 77; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX P45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, scleroderma, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia

Query Match 92.3%; Score 12; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UUCGUCUUGCA 13
Db 1 TTGCTTTGCA 12

RESULT 6
AAFS1539
ID AAF51539 standard; DNA; 15 BP.
XX
XX AAF51539;

XX 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #2499.
 XX
 KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KM cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryriasis;
 KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KM growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KM hyperneovascular condition; hyperplasia; kidney disease;
 KM neovascular condition of the retina; ss.
 XX Homo sapiens.
 XX OS
 XX W0200078341-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX PF
 XX 21-JUN-1999; 99US-0140345P.
 XX PR
 XX (MURDOCH CHILDRENS RES INST.
 XX PA
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX PI
 XX WPI; 2001-041421/05.
 XX DR
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX PT
 XX
 XX Example 8; Page 77; 201pp; English.
 XX PS
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisense
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX F45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, pteryriasis, ruba, pilaris, serborrhea, keloids, keratosis, a
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX CC
 XX
 XX Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
 XX SQ
 XX
 XX Query Match 92.3%; Score 12; DB 1; Length 15;
 XX Best Local Similarity 50.0%; Pred. No. 2.5;
 XX Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CUUGUCUUGC 12
 XX |::||::||
 XX DB 4 CTTGCTCTTTC 15

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 XX Saccharomyces cerevisiae.
 XX OS
 XX W0200077214-A2.
 XX
 XX 21-DEC-2000.
 XX PD
 XX 14-JUN-2000; 2000WO-US016223.
 XX PF
 XX 16-JUN-1999; 99US-00335032.
 XX PR
 XX (UTJO) UNIV JOHNS HOPKINS.
 XX PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX PI
 XX WPI; 2001-061874/07.
 XX DR
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX PT gene expression (SAGE) tags, useful for studying, monitoring and
 XX PT affecting phases of the cell cycle.
 XX PT
 XX Example; Page 188; 419pp; English.
 XX PS
 XX The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX previously assigned open reading frame) or nonannotated ORF) genes
 XX comprising a SAGE (serial analysis of gene expression) tag. Also
 XX described are: (1) a method (M1) of using NORF genes to affect the cell
 XX cycle comprising administering a NORF gene whose expression varies by at
 XX least 10% between any two phases of the cell cycle selected from log
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX cell; and (b) monitoring expression of a NORF gene whose expression
 XX varies as in M1, where a test substance which modifies the expression of
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX identifying human genes which are involved in cell cycle progression
 XX comprising contacting human DNA with a probe which comprises at least 10
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX and (4) a method (M4) for identifying a candidate drug as a member of a
 XX class of drugs having a characteristic effect on gene expression in a
 XX yeast cell comprising contacting a yeast cell with a candidate drug and
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX expression is affected by the class of drugs. The NORF genes may be used
 XX to study, monitor and affect phases of the cell cycle, the differentially
 XX expressed genes may be used as markers of phases of the cell cycle. The
 XX methods may be used to identify candidate drugs which affect the cell
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 XX represent SAGE tags used in the exemplification of the present invention.
 XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX method, in the exemplification of the present invention
 XX CC
 XX
 XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
 XX SQ
 XX
 XX Query Match 76.9%; Score 10; DB 1; Length 10;
 XX Best Local Similarity 40.0%; Pred. No. 7.7;
 XX Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 CUUGUCUUU 10
 XX |::||::||
 XX DB 10 CTTGCTTTT 1

RESULT 7
 AAF38544/c
 ID AAF38544 standard; DNA; 10 BP.
 XX
 XX AAF38544;
 XX AC
 XX 23-MAR-2001 (first entry)
 XX DT
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5283.
 XX DE

RESULT 8
 AAF41570
 ID AAF41570 standard; DNA; 10 BP.
 XX
 XX AAF41570;
 XX AC
 XX

DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8309.
 DE
 XX
 KM Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; de.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000MO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 296; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10 between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 69.2%; Score 9; DB 1; Length 10;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CUCGUCUCU 9
 Db 1 CTTGCTCTT 9
 RESULT 9
 AAF35016
 ID AAF35016 standard; DNA; 10 BP.

XX AAF35016;
 AC
 XX
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1755.
 DE
 XX
 KM Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; de.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000MO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 62; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10 between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 69.2%; Score 9; DB 1; Length 10;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 2 UUCGUCUUU 10
 Db 1 TTGCTCTTT 9

XX Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;
 SQ Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 13;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UCGUCUUUGC 12
 Db 1 TCGCTTTTC 10

RESULT 14
 AAF42256/c
 ID AAF42256 standard; DNA; 10 BP.
 XX AAF42256;
 AC
 XX
 XX 23-MAR-2001 (first entry)
 DT
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8995.
 XX
 KM Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KM not previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 PF 14-JUN-2000; 2000WO-US016223.
 PR 16-JUN-1999; 99US-00335032.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 321; 419pp; English.

The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064

CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UCGUCUUUGC 12
 Db 10 TCGCTTTTC 1

RESULT 15
 AAF36161/c
 ID AAF36161 standard; DNA; 10 BP.
 XX AAF36161;
 AC
 XX
 XX 23-MAR-2001 (first entry)
 DT
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2900.
 XX
 KM Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KM not previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 PF 14-JUN-2000; 2000WO-US016223.
 PR 16-JUN-1999; 99US-00335032.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 103; 419pp; English.

The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 CC XX

SO Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 13;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 CUCGUCUUC 10
 Db 10 CTTGCTTTG 1

RESULT 16
 AAF3800
 ID AAF3800 standard; DNA; 10 BP.
 AC AAF3800;
 XX
 DT 23-MAR-2001 (first entry)
 XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11939.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN MO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000MO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 376; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 CC XX

SO Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 30.0%; Pred. No. 13;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 2 UUCGUCUUC 11
 Db 1 TTGCTTTG 10

RESULT 17
 AAF38546/c
 ID AAF38546 standard; DNA; 10 BP.
 AC AAF38546;
 XX
 DT 23-MAR-2001 (first entry)
 XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5285.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN MO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000MO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 188; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX
 SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 13;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 CUCGUCUUTU 10
 |||::|
 10 CTCGCTCTT 1

Db

RESULT 18
 AAF40426/c
 ID AAF40426 standard; DNA; 10 BP.
 XX
 AC AAF40426;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7165.
 XX
 KM Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KM serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 255; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX
 SQ Sequence 10 BP; 7 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 30.0%; Pred. No. 13;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 2 UUCGUCUUG 11
 ::|||::|
 10 TTCCTTTTG 1

Db

RESULT 19
 ABR36059
 ID ABR36059 standard; DNA; 10 BP.
 XX
 AC ABR36059;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human LIPF gene polymorphism detection oligonucleotide primer #34.
 XX
 KM Human; lipase; hormone sensitive; LIPF; isogene; obesity; male sterility;
 KM polymorphism; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200240502-A2.
 PD 23-MAY-2002.
 XX
 PF 16-NOV-2001; 2001WO-US043518.
 XX
 PR 16-NOV-2000; 2000US-0249302P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AB, Bentivegna SC, Chew A, Koshy B, Rounds E;
 DR WPI; 2002-519369/55.
 XX
 PT Novel genetic variants of lipase, Hormone-Sensitive isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with LIPF activity, e.g. obesity and male sterility.
 XX
 PS Claim 17; Page 16; 142pp; English.

XX The present invention relates to a new polynucleotide comprising a
 CC nucleotide sequence which comprises lipase, hormone sensitive (LIPF)
 CC isogenes. The invention is useful in screening for drugs targeting LIPF
 CC isogenes that are useful for treating obesity and male sterility. The
 CC methods of the invention are useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with LIPF activity. The polynucleotide
 CC is useful in studying the expression and function of LIPF, and in
 CC expressing LIPF protein for use in screening for candidate drugs to treat
 CC diseases related to LIPF activity. It is also useful in studying the
 CC effect of the variation on the biological activity of LIPF as well as on

CC the binding affinity of candidate drugs targeting LIPB for the treatment
CC of obesity and male sterility. The invention is useful for studying the
CC expression of LIPB isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against LIPB protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating obesity and male sterility
CC in a biological system. The present nucleic acid sequence represents one
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
CC used in the invention to detect polymorphisms in the human LIPB gene
SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUUG 11
: |||::||
Db 1 TCCGCTTTG 10

RESULT 20

ID ADI13726 standard; DNA; 10 BP.

AC ADI13726;

DT 22-APR-2004 (first entry)

DE Cytoplasmic tumour endothelial marker standard tag SEQ ID NO:101.

XX tumour endothelial marker; TEM; endothelial cell regulation;

KW neovascularization; neovascularization; neovascularization; tumour; wound healing;

KW cytochrome; cytochrome; cytochrome; cytochrome; cytochrome; cytochrome;

XX Homo sapiens.

OS Synthetic.

PN WO2004005883-A2.

PD 15-JAN-2004.

PF 02-JUL-2003; 2003WO-US016250.

PR 02-JUL-2002; 2002US-0393023P.

PR 01-APR-2003; 2003US-0458964P.

XX (UWJO) UNIV JOHNS HOPKINS.

PI St Croix B, Kinzler KW, Vogelstein B;

DR WPI; 2004-142995/14.

XX Use of tumor endothelial marker proteins for inhibiting neovascularization,

PT screening for neovascularization, promoting neovascularization, identifying

PT candidate drugs for treating tumors or promoting wound healing.

XX Disclosure; SEQ ID NO 101; 113pp; English.

XX The present invention describes the use of tumour endothelial marker

CC (TEM) proteins for identifying a ligand involved in endothelial cell

CC regulation, inhibiting neovascularization, screening for neovascularization,

CC promoting neovascularization, identifying candidate drugs for treating

CC tumours or promoting wound healing or identifying endothelial cells. Also

CC described: (1) identification of a ligand involved in endothelial cell

CC regulation; (2) inhibiting neovascularization; (3) promoting neovascularization

CC in a patient; (4) screening for neovascularization in a patient; (5)

CC identify candidate drugs for treating tumours or promoting wound healing;

CC and (6) identifying endothelial cells. TEM proteins have cytochrome and

CC ligand involved in endothelial cell regulation, inhibiting

CC neovascularization, screening for neovascularization, promoting

CC neovascularization, identifying candidate drugs for treating tumours or

CC promoting wound healing or identifying endothelial cells. The present
CC sequence represents a cytoplasmic tumour endothelial marker standard tag
CC oligonucleotide, which is used in the exemplification of the present
CC invention.

SQ Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UUCGUCUUG 12
: |||::||
Db 1 TCCGCTTTG 10

RESULT 21

ID ADU50908 standard; DNA; 10 BP.

AC ADU50908;

DT 27-JAN-2005 (first entry)

DE Analyte detection-related human p53-targeting oligonucleotide probe #8.

XX analyte detection; probe; seq. p53.

OS Homo sapiens.

OS Synthetic.

PN WO2004097371-A2.

PD 11-NOV-2004.

PF 26-APR-2004; 2004WO-US012916.

PR 25-APR-2003; 2003US-0465336P.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Schmid MJ, Willson GC;

DR WPI; 2005-012657/01.

XX Analyte detection device, has sensing elements coupled with probes that

PT are capable of producing signal when analyte interacts with probe and

PT determining identity of analyte based on signal produced by sensing

PT element.

XX Example; Fig 2; 32pp; English.

XX This invention relates to a novel analyte detection device, having

CC several sensing elements, where one or more probes are coupled to each of

CC the sensing elements, and where at least one of the probes is configured

CC to interact with an analyte, and where at least one sensing element

CC produces a signal when the analyte interacts with a probe, and where

CC sensing elements produce detectable signals in predetermined pattern that

CC represents a code that identifies analyte. The invention is useful for

CC analyzing analytes such as DNA, RNA, proteins, enzymes, oligopeptides,

CC antigens, antibodies or organic molecules. The present sequence is that

CC of an oligonucleotide probe which targets a region of the human p53 gene

CC and which was used in the exemplification of the invention.

SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUUG 11
: |||::||
Db 1 TCCGCTTTG 10

```

RESULT 22
AAZ82055/c
ID AAZ82055 standard; DNA; 10 BP.
XX
AC AAZ82055;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1289.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 93; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
.OY 2 UUCGUCUU 9

```

```

Db 9 TTCGCTTT 2
::|||::
9 TTCGCTTT 2

RESULT 23
AAH63934
ID AAH63934 standard; cDNA; 10 BP.
XX
AC AAH63934;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 774.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
XX WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 56; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
XX
Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
.OY 3 UCGUCUUU 10
Db 1 TTCGCTTT 8
::|||::
1 TTCGCTTT 8

RESULT 24
AAF34140/c
ID AAF34140 standard; DNA; 10 BP.
XX
AC AAF34140;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:879.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; de.

```

XX	Saccharomyces cerevisiae.
OS	WO200077214-A2.
XX	
XX	21-DEC-2000.
PD	
XX	14-JUN-2000; 2000WO-US016223.
PF	
XX	16-JUN-1999; 99US-00335032.
PR	
XX	(UYJO) UNIV JOHNS HOPKINS.
PA	
XX	Velculescu V, Vogelstein B, Kinzler K;
PI	
XX	WPI; 2001-061874/07.
DR	
XX	
PT	Yeast gene coding sequences comprising NORF genes with serial analysis of
PT	gene expression (SAGE) tags, useful for studying, monitoring and
PT	affecting phases of the cell cycle.
XX	
PS	Example; Page 31; 419pp; English.
CC	
XX	The present invention describes an isolated DNA molecule comprising a
CC	coding sequence of a yeast gene selected from a group of 745 NORF (not
CC	previously assigned open reading frame; or nonannotated ORF) genes
CC	comprising a SAGE (serial analysis of gene expression) tag. Also
CC	described are: (1) a method (M1) of using NORF genes to affect the cell
CC	cycle comprising administering a NORF gene whose expression varies by at
CC	least 10% between any two phases of the cell cycle selected from log
CC	phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC	antifungal drugs comprising: (a) contacting a test substance with a yeast
CC	cell; and (b) monitoring expression of a NORF gene whose expression
CC	varies as in M1, where a test substance which modifies the expression of
CC	the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC	identifying human genes which are involved in cell cycle progression
CC	comprising contacting human DNA with a probe which comprises at least 10
CC	contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC	and (4) a method (M4) for identifying a candidate drug as a member of a
CC	class of drugs having a characteristic effect on gene expression in a
CC	yeast cell comprising contacting a yeast cell with a candidate drug and
CC	monitoring expression in the yeast cell of at least 1 NORF gene whose
CC	expression is affected by the class of drugs. The NORF genes may be used
CC	to study, monitor and affect phases of the cell cycle, the differentially
CC	expressed genes may be used as markers of phases of the cell cycle. The
CC	method may be used to identify candidate drugs which affect the cell
CC	cycle and for identification of antifungal drugs. AAF33266 to AAF44064
CC	represent SAGE tags used in the exemplification of the present invention.
CC	AAF33262 to AAF33267 represent linker and PCR primers used in the SAGE
CC	method. In the exemplification of the present invention
XX	
XX	Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
XX	
Query Match	61.5%; Score 8; DB 1; Length 10;
Best Local Similarity	50.0%; Pred. No. 15;
Matches 4; Conservative	4; Mismatches 0; Indels 0; Gaps 0;
OY	5 GUCUUGC 12
	:
Db	8 GTCCTTC 1
RESULT 25	
ID	AAF42583
XX	AAF42583 standard; DNA; 10 BP.
XX	
XX	AAF42583;
XX	
XX	23-MAR-2001 (first entry)
XX	
XX	Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10722.
XX	
XX	Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

nor previously assigned open reading frame; nonannotated ORF, SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; ds.
 OS *Saccharomyces cerevisiae*.
 PN MO200077214-A2.
 XX
 XX
 PD 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 PR
 PA (UTJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 332; 419pp; English.
 PS
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33362 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 6 UCUDUGCA 13
 :||:||||
 Db 3 TCTTTGCA 10
 RESULT 26
 AAF37269/c
 ID AAF37269 standard; DNA; 10 BP.
 XX AAF37269;
 AC
 XX 23-MAR-2001 (first entry)
 XT

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4008.
 XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; de.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN W0200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 143; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 6 UCUUUGCA 13
 Db 9 TCTTGGCA 2
 XX
 RESULT 27
 ID AAF38836 standard; DNA; 10 BP.
 XX
 AC AAF38836;

XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5575.
 XX
 KM Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KM linker; PCR primer; de.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN W0200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 199; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 15;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 UUCGUCUU 9
 Db 8 TTCGCTCT 1
 XX
 RESULT 28
 ID AAF42254/c

ID	AAFA42254 standard; DNA; 10 BP.
XX	AAFA42254 standard; DNA; 10 BP.
AC	AAFA42254;
XX	
DT	23-MAR-2001 (first entry)
XX	
DE	Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8993.
KM	
KW	Yeast; <i>Saccharomyces cerevisiae</i> ; characterisation; cell cycle; NORF; not previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
XX	
OS	<i>Saccharomyces cerevisiae</i> .
XX	
PN	MO200077214-A2.
PD	
XX	
PD	21-DEC-2000.
XX	
PF	14-JUN-2000; 2000MO-US016223.
XX	
PR	16-JUN-1999; 99US-00335032.
XX	
PA	(UYJO) UNIV JOHNS HOPKINS.
XX	
PI	Velculescu V, Vogelstein B, Kinzler K;
XX	
DR	WPI; 2001-061874/07.
PT	
PT	Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
XX	
PS	Example; Page 321; 419pp; English.
XX	
CC	The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
XX	
SO	Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
XX	
Query Match	61.5%; Score 8; DB 1; Length 10;
Best Local Similarity	50.0%; Pred. No. 15;
Matches	4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
5 GUCUUGC 12	
8 GUCUUGC 1	

Query Match	61.5%	Score 8	DB 1	Length 10
Best Local Similarity	37.5%	Pred. No. 15		
Matches	3	Conservative	5	Mismatches
			0	Indels
			0	Gaps
			0	

3

UCGUCUUU 10

Db 10 TCGCTTT 3

RESULT 30

AAFA3668 ID AAF43668 standard; DNA; 10 BP.

XX AAF43668;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11807.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
linker; PCR primer; de.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 371; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 15;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UCUCUGCA 13

Db 2 TCTTGC 9

RESULT 31

AAFA0632/c ID AAF40632 standard; DNA; 10 BP.

XX AAF40632;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7371.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KM nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
linker; PCR primer; de.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 263; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUCGUCU 8
 Db 9 CTTGCTCT 2

RESULT 32

ACC69588/c
 ID ACC69588 standard; DNA; 10 BP.

XX ACC69588;

XX 16-JUL-2003 (first entry)

XX D. melanogaster 42 bp deletion flanking oligonucleotide SEQ ID NO:20.

XX Drosophila; insecticide; cyp6g1; pesticide; ss.

XX Drosophila melanogaster.

XX Synthetic.

XX MO2003025223-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002MO-GB004213.

XX 20-SEP-2001; 2001GB-00022693.

XX (UYBA-) UNIV BATH.

XX French-Constant RH; Daborn PJ;

XX WPI; 2003-333171/31.

XX Use of a cell, cell line or organism in which the activity of Drosophila melanogaster gene cyp6g1, is increased relative to wild type activity of cyp6g1, for the screening of putative pesticides.

XX Claim 12; Page 59; 85pp; English.

XX The present invention describes the use of a cell, cell line or organism (collectively referred to as (1)) in which the activity of the Drosophila melanogaster gene cyp6g1, its derivatives or fragments, is increased relative to wild type activity of cyp6g1, for the screening of putative pesticides. Also described: (1) testing a putative pesticide for its potential resistance, by contacting (1) and detecting any detrimental effect on (1); (2) testing a putative pesticide for its potential resistance, by contacting (1) comprising a transposable element and detecting any detrimental effect on (1); and (3) a pesticide whose activity is detected by the above method; (1) is useful in the screening of putative pesticides. The present sequence represents an oligonucleotide which flanks a 42 bp deletion of Drosophila melanogaster cyp6g1, which is used in an example from the present invention

Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 15;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 UUCGUCU 9
 Db 10 TTGCTCT 3

RESULT 33
 AAD08670
 ID AAD08670 standard; DNA; 9 BP.

XX AAD08670;
 AC
 XX 04-SEP-2001 (first entry)

XX Human OY-TES-1 full length cDNA isolating 5' RACE-PCR primer #2.

XX Human; cytostatic; fibrosarcoma cancer; cancer associated antigen; RACE; rapid amplification of cDNA end; gene therapy; vaccine; PCR primer; ss.

XX Homo sapiens.

XX MO200140271-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000MO-US032750.

XX 01-DEC-1999; 99US-0168353P.

XX 26-APR-2000; 2000US-00559013.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Ono T; Nakayama E;

XX WPI; 2001-397941/42.

XX Isolated polypeptide, useful in treating disorders such as cancer, is encoded by a nucleic acid (NA) Group 3 or 4 molecule.

XX Example 2; Page 70; 127pp; English.

XX The invention relates to cancer associated antigens and their nucleic acids which are expressed in methyloanthrene-induced fibrosarcoma cancer cells from mice. Cancer associated antigens and a pharmaceutical composition containing nucleic acid molecules encoding cancer associated antigens are used to treat a condition e.g. cancer. Cancer associated antigens, the nucleotides encoding them, antibodies against them and the pharmaceutical compositions comprising them are useful for diagnosing, monitoring and treating the diseases characterised by the expression of one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for research purposes. Cancer associated antigens DNA is also useful in gene therapy. The present sequence is 5' RACE (rapid amplification of cDNA end) PCR primer used for isolating human full length OY-TES-1 cDNA

Query Match 56.3%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 77;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUUCGUCU 9
 Db 1 CTTGCTCT 9

RESULT 34

ABK29982
 ID ABK29982 standard; DNA; 8 BP.

XX ABK29982;

XX 23-APR-2002 (first entry)

XX Hepatitis B virus (HBV) domain 12-1 wild type.

XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;

XX HBV promoter; vancomycin-resistant enterococci promoter; VAB promoter;

XX vanH promoter; androgen receptor promoter; AR promoter;

XX human epidermal growth factor receptor 2 promoter; her2 promoter;

XX beta lactamase promoter; B1a promoter; transgene; cancer; breast cancer;

XX colon cancer; immunological disorder; prostate cancer; cytostatic;

XX autoimmune disease; HBV pre-S promoter; HBV-X promoter;

KM Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KM gene expression modulator; multiple sclerosis; MS;
 KM chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KM systemic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KM familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KM transgenic; ds.
 XX
 OS Hepatitis B virus.
 XX
 PN MO200194600-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 06-JUN-2001; 2001MO-US018343.
 XX
 PR 06-JUN-2000; 2000US-0209549P.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Kim JP, Starr DB, Tam AW, Laurence ME, Michelotti EF;
 PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Shepard LT;
 PI Lim MY, Bruce TW;
 XX
 DR WPI; 2002-130595/17.
 XX
 PT New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.
 PS
 PS Example 3; Page 43; 95pp; English.
 XX
 CC The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This represents the wild type sequence of a promoter region used
 CC in the invention to create mutant promoter fragments to determine the
 CC regulatory regions involved in gene expression, described in the method
 CC of the invention
 XX
 SQ Sequence 8 BP; 0 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 53.8%; Score 7; DB 1; Length 8;
 Best Local Similarity 42.9%; Pred. No. 87;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 GUCUUUG 11
 |.:|.:|
 Db 1 GTCCTTG 7

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:03:21 / Search time 0.001 Seconds
(without alignments)
3.848 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 17 seqs, 148 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 17 summaries

Database: rgedb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	1	AR407995
2	8	61.5	10	1	AR303335
3	8	61.5	10	1	AX152859
4	8	61.5	10	1	AX301317
5	8	61.5	10	1	AX806339
6	7.4	56.9	9	1	CS071888
7	7.4	56.9	9	1	CS133987
8	7	53.8	7	1	CQ766095
9	7	53.8	7	1	CQ766096
10	7	53.8	7	1	CQ766097
11	6.4	49.2	8	1	CQ924619
12	6.4	49.2	8	1	E02034
13	6.4	49.2	8	1	AX003298
14	6.4	49.2	8	1	AX104953
15	6.4	49.2	8	1	AX211691
16	6.4	49.2	8	1	AX358376
17	6.4	49.2	8	1	AX358378

ALIGNMENTS

RESULT 1
LOCUS AR407995 13 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 88 from patent US 6632057.
ACCESSION AR407995
VERSION AR407995.1 GI:40157982
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)

AUTHORS Fauchet, C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 88 14-OCT-2003;
GPI Aerospace; Paris;

FEATURES
source

Location/Qualifiers
1..13
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 100.0%; Score 13; DB 1; Length 13;
Best Local Similarity 53.8%; Pred. No. 0.28;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

CY 1 CUUCGUCUUUGCA 13
DB 1 CTTCTCTTTGCA 13

RESULT 2

AR303335 10 bp DNA linear PAT 12-JUN-2003
LOCUS AR303335
DEFINITION Sequence 60 from patent US 6544736.
ACCESSION AR303335
VERSION AR303335.1 GI:31692111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 10)
AUTHORS Shimamoto, A., Furutachi, Y., Shibata, Y., Funaki, H., Ohara, E. and
Watanishi, M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544735-A 60 08-APR-2003;
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
Tokyo;
JPX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY 5 GUCUTUUGC 12
DB 2 GTCTTTGC 9

RESULT 3

AX152859 10 bp DNA linear PAT 22-JUN-2001
LOCUS AX152859
DEFINITION Sequence 774 from Patent WO0138577.
ACCESSION AX152859
VERSION AX152859.1 GI:14534510
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 774 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 2;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 3 UCGUCUU 10
 Db 1 TCGTCTT 8

RESULT 4
 AX301317 10 bp DNA linear PAT 30-NOV-2001
 LOCUS Sequence 31 from Patent WO0185941.
 DEFINITION AX301317
 ACCESSION AX301317.1 GI:17382400
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1
 Verveeg, R. and Caron, H.N.
 MYC targets
 TITLE Patent: WO 0185941-A 31.15-NOV-2001.
 JOURNAL Academiisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
 FEATURES 1.10
 source /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 2;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 3 UCGUCUU 10
 Db 1 TCGTCTT 8

RESULT 5
 AX806339 10 bp DNA linear PAT 25-NOV-2003
 LOCUS Sequence 20 from Patent WO03025223.
 DEFINITION AX806339
 ACCESSION AX806339.1 GI:38523027
 VERSION
 KEYWORDS
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 French-Constant, R.H. and Daborn, P.J.
 TITLE Improvements in or relating to insecticide screening
 JOURNAL Patent: WO 03025223-A 20 27-MAR-2003;
 UNIVERSITY OF BATH (GB)
 FEATURES 1.10
 source location/Qualifiers
 /organism="Drosophila melanogaster"
 /mol_type="unassigned DNA"
 /db_xref="taxon:7227"
 /note="Sequence flanking 42 bp deletion in 5'UTR"

Query Match 61.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 2;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 2 UUGUCUU 9
 Db 10 TTCGTCTT 3

RESULT 6
 CS071888 9 bp DNA linear PAT 05-MAY-2005
 LOCUS Sequence 36 from Patent WO2001040271.
 DEFINITION CS071888
 ACCESSION CS071888.1 GI:63089211
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1
 Ono, T. and Nakayama, E.
 TITLE Cancer associated antigens and uses therefor
 JOURNAL Patent: WO 2001040271-A 36 07-JUN-2001;
 Ludwig Institute for Cancer Research (US)
 FEATURES 1.9
 source location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 56.9%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 12;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CUUGUCUU 9
 Db 1 CTTCGTGT 9

RESULT 7
 CS133987 9 bp DNA linear PAT 02-AUG-2005
 LOCUS Sequence 529 from Patent WO2005058479.
 DEFINITION CS133987
 ACCESSION CS133987.1 GI:71793536
 VERSION
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
 Morgan, B.
 TITLE Methods for synthesis of encoded libraries
 JOURNAL Patent: WO 2005058479-A 529 30-JUN-2005;
 Praeclis Pharmaceuticals Inc. (US)
 FEATURES 1.9
 source location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic construct"

Query Match 56.9%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 12;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 UCGUCUU 11
 Db 9 TCGTCGTG 1

RESULT 8
 CQ766095 7 bp DNA linear PAT 03-MAR-2004
 LOCUS Sequence 56 from Patent WO2004005547.
 DEFINITION CQ766095
 ACCESSION CQ766095.1 GI:44908355
 VERSION
 KEYWORDS
 SOURCE synthetic construct

```

ORGANISM    synthetic construct
REFERENCE    other sequences; artificial sequences.
1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 56 15-JAN-2004;
              IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     location/Qualifiers
source       1..7
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="HS consensus sequence"

Query Match      53.8%; Score 7; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 15;
Matches          3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY              4 CGUCUUU 10
Db              7 CGTCTTT 1

RESULT 9
LOCUS          CO766096
DEFINITION     Sequence 57 from Patent WO2004005547.
ACCESSION      CO766096
VERSION         CO766096.1 GI:44908356
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE        other sequences; artificial sequences.
1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 57 15-JAN-2004;
              IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     location/Qualifiers
source       1..7
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="HS consensus sequence"

Query Match      53.8%; Score 7; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 15;
Matches          3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY              4 CGUCUUU 10
Db              7 CGTCTTT 1

RESULT 10
LOCUS          CO766097/c
DEFINITION     Sequence 58 from Patent WO2004005547.
ACCESSION      CO766097
VERSION         CO766097.1 GI:44908357
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE        other sequences; artificial sequences.
1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 58 15-JAN-2004;
              IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     location/Qualifiers
source       1..7
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              /mol_type="unassigned DNA"

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Query Match      53.8%; Score 7; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 15;
Matches          3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY              4 CGUCUUU 10
Db              7 CGTCTTT 1

RESULT 11
LOCUS          CO924619
DEFINITION     Sequence 3 from Patent WO2004097043.
ACCESSION      CO924619
VERSION         CO924619.1 GI:56214216
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE        other sequences; artificial sequences.
1
AUTHORS      Douglas,K.T., Bichenkova,E.V., Savage,H. and Sardarian,A.U.
TITLE        Exciplexes
JOURNAL      Patent: WO 2004097043-A 3 11-NOV-2004;
              THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
FEATURES     location/Qualifiers
source       1..8
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="8mer labelled probe"

Query Match      49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 13;
Matches          4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY              5 GUCUUGC 12
Db              1 GTCCTAGC 8

RESULT 12
LOCUS          E02034/c
DEFINITION     DNA sequence before initiation codon containing initiation codon.
ACCESSION      E02034
VERSION         E02034.1 GI:22026665
KEYWORDS      JP 1989196296-A/1.
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS      Sakurai,T., Naruto,M. and Ozawa,H.
TITLE        MANIPESTATION VECTOR FOR ANIMAL CELL
JOURNAL      Patent: JP 1989196296-A 1 08-AUG-1989;
              TORAY IND INC
COMMENT       OS Artificial gene
              OC Artificial sequence; Genes.
              PN JP 1989196296-A/1
              PD 08-AUG-1989
              PF 29-JAN-1988 JP 1988020174
              PI SAKURAI TORU, NARUTO MASANOBU, OZAWA HITOSHI
              PC C12N15/00;
              CC strandedness: Single;
              CC topology: linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH key Location/Qualifiers
              FT CDS 6..>8
              FT /Codon_start=1.

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FEATURES
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        1..8
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
    49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 13;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY
    4 CGUCGUCU 11
    |:|:|:|
    8 CATCTTG 1
    Db

RESULT 13
AX003298      8 bp      DNA      linear      PAT 07-SEP-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Circovirus
    Viruses; ssDNA viruses; Circoviridae.
REFERENCE
    1 (bases 1 to 8)
    Hutet,E., Albina,E., Arnaud,C., Cariolet,R., Jestin,A., Le,C.P.,
    Madec,P., Mahe,D., Blanchard,P. and Truong,C.
    Circovirus sequences related to piglet weight loss disease (pwl)
    Patent: WO 9929871-A 33 17-JUN-1999;
    HUTET EVELYNE (FR); ALBINA EMMANUEL (FR); ARNAUD CLAIRE (FR);
    CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
    FRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
    CATHERINE (FR); VETERINAIRES ET ALIMENTAIRES C (FR)
FEATURES
    source
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        /organism="Circovirus"
        /mol_type="genomic DNA"
        /db_xref="taxon:39725"

Query Match
    49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 13;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY
    2 UUCGUCUU 9
    :|:|:|:
    1 TCCGCTT 8
    Db

RESULT 14
AX104953      8 bp      DNA      linear      PAT 30-APR-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
    1 (bases 1 to 8)
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
    Immunostimulatory nucleic acids
    Patent: WO 012972-A 1145 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
    GmbH (DE)
FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
    49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 13;

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Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY
    3 UCGUCUUU 10
    :|:|:|:
    1 TCGGCTT 8
    Db

RESULT 15
AX211691      8 bp      mRNA      linear      PAT 06-SEP-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
    1 (bases 1 to 8)
    Vanderhaeghen,R. and van Lijsebetens,M.
    Plant internal ribosome entry segment
    Patent: WO 0159138-A 21 16-AUG-2001;
    Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
    source
        1..8
        /organism="synthetic construct"
        /mol_type="mRNA"
        /db_xref="taxon:32630"
        /note="effector sequence"

Query Match
    49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 13;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY
    1 CUUCGUCU 8
    |:|:|:|
    1 CTCTCTT 8
    Db

RESULT 16
AX358376      8 bp      mRNA      linear      PAT 13-FEB-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
    1
    Wang,D.
    Genetic vaccine that mimics natural viral infection and induces
    long-lasting immunity to pathogens
    Patent: WO 0191536-A 3 06-DEC-2001;
    Genphar, Inc. (US)
FEATURES
    source
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        /note="modified RNA editing site"

Query Match
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Best Local Similarity 25.0%; Pred. No. 13;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY
    2 UUCGUCUU 9
    :|:|:|:
    1 TTCTCTT 8
    Db

RESULT 17
AX358378/c    8 bp      DNA      linear      PAT 13-FEB-2002
LOCUS

```

DEFINITION Sequence 5 from Patent WO0191536.
 ACCESSION AX358378
 VERSION AX358378.1 GI:18675014
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Wang, D.
 TITLE Genetic vaccine that mimics natural viral infection and induces
 long-lasting immunity to pathogens
 JOURNAL Patent: WO 0191536-A 5 06-DEC-2001;
 Genphar, Inc. (US)
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="DNA of modified RNA editing site."
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 Best Local Similarity 25.0%; Pred. No. 13;
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 2 UUCGUCUU 9
 ::|:|::
 Db 8 TTCTTCTT 1

Search completed: September 1, 2006, 12:03:21
 Job time : 0.001 secs

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QY 3 UCGUCUUC

Db 1 TCGTCTT 8

RESULT 4

US-10-293-222-31
; Sequence 31, Application US/10293222
; Publication No. US2004003932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293, 222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-31

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCGUCUUU 10
:|:|:|:
Db 1 TCGTCTT 8

Search completed: September 1, 2006, 12:06:55
Job time : 0.001 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:07:57 ; Search time 0.001 Seconds
(without alignments)
1.222 Million cell updates/sec

Title: us-09-847-601b-88

Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 9 segs, 47 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 9 summaries

Database : rscdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5	38.5	5	1	CF332399
C 2	5	38.5	6	1	CA850767
C 3	5	38.5	6	1	DU784614
C 4	4	30.8	5	1	CL658581
C 5	4	30.8	5	1	CL667999
C 6	4	30.8	5	1	CL685291
C 7	4	30.8	5	1	DU643362
C 8	4	30.8	5	1	DU643819
C 9	4	30.8	5	1	DX081067

ALIGNMENTS

RESULT 1
CF332399/c 5 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-007.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-007, mRNA
Sequence.

ACCESSION CF332399
VERSION CF332399
KEYWORDS
SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Euharoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 5)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, U.K., Kim, Y.-K., and Nam, B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT

Contact: Nam B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..5
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="NACL--08-007"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 38.5%; Score 5; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 0;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Oy 6 UCUCU 10
|:::
Db 5 TCTTT 1

RESULT 2
CA850767/c 6 bp mRNA linear EST 01-AUG-2003
LOCUS D06C11 C11.05.ab1 CDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION CDNA clone D06C11 5, mRNA sequence.

ACCESSION CA850767
VERSION CA850767.1 GI:33387560
KEYWORDS
SOURCE

ORGANISM Glycine max (soybean)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.

REFERENCE 1 (bases 1 to 6)
Alkharouf, N., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL Genome 47 (2), 380-388 (2004)
PUBMED 15060591

COMMENT

Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA

Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.ars.usda.gov.
Location/Qualifiers

FEATURES
source

1..6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06C11"
/tissue_type="Roots"
/dev_stage="Seedlings"
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/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days post invasion."

Query Match 38.5%; Score 5; DB 1; Length 6;

Best Local Similarity 50.0%; Pred. No. 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 UUCUC 7
Db 6 TTCGC 1

RESULT 3
DUT84614 6 bp DNA linear GSS 27-JAN-2006
LOCUS HF500_42_54TR HF500_10-06-02 uncultured marine microorganism
DEFINITION HF500_10-06-02 genomic clone HF500_42_54TR, genomic survey
sequence.

ACCESSION DUT84614.1 GI:85798909
VERSION DUT84614
KEYWORDS GSS.

SOURCE uncultured marine microorganism HF500_10-06-02
ORGANISM uncultured marine microorganism HF500_10-06-02
REFERENCE unclassified sequences; environmental samples.
1 (bases 1 to 6)

AUTHORS Delong, E. F., Preston, C. M., Mincer, T., Rich, V., Hallam, S. J.,
Frigaard, N. U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S. W.
and Karl, D. M.

TITLE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior

JOURNAL Science (2006) In press
COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tjiana Glavinadeliro, David Bruce, Paul Richardson
and Edward DeLong

US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679

Email: pkrichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 500 m Temperature: 7.25 C
Salinity: 34.07 psu Oxygen: 118.0 umol/kg
Class: fosmid ends.
Location/Qualifiers

FEATURES
source 1..6

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/note="Vector: pC1FOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 500 m
depth on 10/6/2002. Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 500 m
Temperature: 7.25 C Salinity: 34.07 psu Oxygen: 118.0
umol/kg"

Query Match 38.5%; Score 5; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 0;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUCUC 8
Db 1 CUCUC 5

RESULT 4
CL658581 5 bp DNA linear GSS 09-JUL-2004
LOCUS CL658581
DEFINITION PRI0131d_E08 - PRI0131d.B21 (5) Mixed stage fosmid library of P.

ACCESSION CL658581.1 GI:50141602
VERSION CL658581
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus

REFERENCE Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
1 (bases 1 to 5)
Appabds: an Acedb database for the nematode satellite organism
Nemodiplogasteridae; Pristionchus.

AUTHORS Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
TITLE Appabds: an Acedb database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447

COMMENT Contact: Sommer RJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers

FEATURES
source 1..5

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pB1FOS-5 Fosmid vector"

Query Match 30.8%; Score 4; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUCUC 4
Db 4 CTC 1

RESULT 5
CL667999 5 bp DNA linear GSS 09-JUL-2004
LOCUS CL667999
DEFINITION PRI0156c_D12 - PRI0156c.B21 (5) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

ACCESSION CL667999.1 GI:50162794
VERSION CL667999
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus

REFERENCE Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
1 (bases 1 to 5)
Appabds: an Acedb database for the nematode satellite organism
Nemodiplogasteridae; Pristionchus.

AUTHORS Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
TITLE Appabds: an Acedb database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447

COMMENT Contact: Sommer RJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.

Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBplfos-5 Fosmid vector"

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Best Local Similarity 25.0%; Pred. No. 0;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 UUCG 11
:::
Db 2 TTGG 5

RESULT 6
LOCUS CL685291 5 bp DNA linear GSS 09-JUL-2004
DEFINITION PR10140d.C11.2 - PR10140d.BR (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL685291 GI:50193442
VERSION GSS.
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 5)
Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcceD database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBplfos-5 Fosmid vector"

Query Match 30.8%; Score 4; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 UUCG 5
:::
Db 1 TTGG 4

RESULT 7
LOCUS DU643362/c 5 bp DNA linear GSS 27-OCT-2005

DEFINITION Cluffi-HIV-293T-wt-2-111C2.M13R Human Integration Site
Library-Cluffi-HIV-293T-wt Homo sapiens genomic, genomic survey sequence.
LOCUS DU643362
ACCESSION DU643362.1 GI:78205732
VERSION GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5)
Cluffi,A., Llano,M., Poeschla,E., Hoffmann,C., Leipziger,J., Shinn,P., Ecker,J.R. and Bushman,F.D. A role for LEDGF/p75 in targeting HIV DNA integration Nat. Med. (2005) In press
JOURNAL Contact: Bushman FD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
The Hg17 (May 2004) freeze of the human genome was used.
Class: Shotgun.
Location/Qualifiers
1. .5
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/cell_type="293T"
/clone_lib="Human Integration Site
Library-Cluffi-HIV-293T-wt"
/note="Sequences cloned using TOPO vectors."

Query Match 30.8%; Score 4; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GUCU 8
:::
Db 5 GTCT 2

RESULT 8
LOCUS DU643819/c 5 bp DNA linear GSS 27-OCT-2005
DEFINITION Cluffi-HIV-293T-wt-2-111C2.M13F Human Integration Site
Library-Cluffi-HIV-293T-wt Homo sapiens genomic, genomic survey sequence.
ACCESSION DU643819
VERSION DU643819.1 GI:78206189
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5)
Cluffi,A., Llano,M., Poeschla,E., Hoffmann,C., Leipziger,J., Shinn,P., Ecker,J.R. and Bushman,F.D. A role for LEDGF/p75 in targeting HIV DNA integration Nat. Med. (2005) In press
JOURNAL Contact: Bushman FD
Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
The Hg17 (May 2004) freeze of the human genome was used.

FEATURES Class: shotgun.
source Location/Qualifiers

1..5
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/cell_type="293T"
/clone_id="Human Integration Site
Library-Cluffi-HIV-293t-wt"
/note="Sequences cloned using TOPO vectors."

Query Match 30.8%; Score 4; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GUCU 8
Db 5 GTCT 2

RESULT 9
DX081067 5 bp DNA linear GSS 10-JAN-2006
LOCUS KRB093N19 KRB, Brassica rapa BamHI BAC library/Brassica rapa
DEFINITION subsp. pekinensis genomic clone KRB093N19, genomic survey
sequence.

ACCESSION DX081067 GI:84775363
VERSION
KEYWORDS

SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KRB) BAC clone

TITLE Unpublished (2005)
JOURNAL
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KRB093N19

Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..5
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KRB093N19"
/lab_host="E.coli DH10B"
/clone_id="KRB, Brassica rapa BamHI BAC library"
/note="Vector: pUCGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chilifu BAC library (KRB BAC) is provided
by Yong-Pyo Lim (CNU)."

FEATURES
source

1..5
/organism="Brassica rapa subsp. pekinensis"
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/sub_species="pekinensis"
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/lab_host="E.coli DH10B"
/clone_id="KRB, Brassica rapa BamHI BAC library"
/note="Vector: pUCGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chilifu BAC library (KRB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 30.8%; Score 4; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 UUCG 5
Db 2 TTGG 5

Search completed: September 1, 2006, 12:07:57
Job time : 0.001 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:05:44 ; Search time 0.001 Seconds
(without alignments)
1.820 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 8 seqs, 70 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database: rntdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	1 US-09-874-601-88	Sequence 88, Appl
2	8	61.5	10	1 US-09-508-753B-60	Sequence 60, Appl
3	6.4	49.2	8	1 US-09-585-599A-3	Sequence 3, Appl
4	6.4	49.2	8	1 US-09-585-599A-5	Sequence 5, Appl
5	6.4	49.2	8	1 US-09-514-245-45	Sequence 45, Appl
6	6.4	49.2	8	1 US-10-327-294-3	Sequence 3, Appl
7	6.4	49.2	8	1 US-10-327-294-5	Sequence 5, Appl
8	6	46.2	7	1 US-09-432-020B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-874-601-88
Sequence 88, Application US/09874601
Patent No. 6632657
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/874.601
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182

SOFTWARE: PatentIn version 3.0
SEQ ID NO 88
LENGTH: 13
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: ()..()
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-88

Query Match 100.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUCGUCUUUGCA 13
DB 1 CUUCGUCUUUGCA 13

RESULT 2

US-09-508-753B-60
Sequence 60, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yoko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masamori WATAHAKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508.753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 60
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-60

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 GUCUUUGC 12
DB 2 GTCCTTGC 9

RESULT 3

US-09-585-599A-3
Sequence 3, Application US/09585599A
Patent No. 6544780
GENERAL INFORMATION:
APPLICANT: Wang, Danler
TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LA
TITLE OF INVENTION: LASTING IMMUNITY TO PATHOGENS
FILE REFERENCE: 22488-706
CURRENT APPLICATION NUMBER: US/09/585.599A
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 8
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: Modified RNA editing site.
US-09-585-599A-3

Query Match 49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUU 9
DB 1 UUCUCUU 8

RESULT 4

US-09-585-599A-5/c
Sequence 5, Application US/09585599A
Patent No. 6544780
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES
FILE REFERENCE: 22488-706
CURRENT APPLICATION NUMBER: US/09/585,599A
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA of modified RNA editing site.
US-09-585-599A-5

Query Match 49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 0;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUU 9
DB 8 TTCTTCTT 1

RESULT 5

US-09-514-245-45
Sequence 45, Application US/09514245
Patent No. 6703023
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emannel
APPLICANT: Le CANH, Pierre
APPLICANT: BLANCHARD, Philippe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAUD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 8
TYPE: DNA
ORGANISM: Type A PWD circovirus
US-09-514-245-45

Query Match 49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 0;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUU 9
DB 1 TCGCTCTT 8

RESULT 6

US-10-327-294-3
Sequence 3, Application US/10327294
Patent No. 6964762
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
FILE REFERENCE: 22488-748
CURRENT APPLICATION NUMBER: US/10/327,294
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 8
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Modified RNA editing site
US-10-327-294-3

Query Match 49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUU 9
DB 1 UUCUCUU 8

RESULT 7

US-10-327-294-5/c
Sequence 5, Application US/10327294
Patent No. 6964762
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
FILE REFERENCE: 22488-748
CURRENT APPLICATION NUMBER: US/10/327,294
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 8
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA of modified RNA editing site
US-10-327-294-5

Query Match 49.2%; Score 6.4; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 0;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 UUCGUCUU 9
DB 8 TTCTTCTT 1

RESULT 8

US-09-432-020B-43/c

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; Sequence 43, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 43
; LENGTH: 7
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CF198 probe; the 3'terminal cytidine contains
; OTHER INFORMATION: an aminopropanol which covalently binds to
; OTHER INFORMATION: the epoxysilaneized glass
US-09-432-020B-43

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Query Match      46.2%; Score 6; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      4 CGUCUU 9
Db      6 CGTCTT 1

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Search completed: September 1, 2006, 12:05:44
 Job time : 0.001 secs

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